IN THE CLAIMS

Claims 1-10 (Cancelled)

Claim 11 (Withdrawn, Currently Amended): A process for the fermentative preparation of an L-amino acid, comprising:

a) fermenting the coryneform bacteria which produce the desired L-amino acid and in which at least the *metE* gene or nucleotide sequences which code for it are enhanced;

b) concentrating the L-amino acid in the medium or in the cells of the bacteria, and

c) isolating the L-amino acid,

wherein said *metE* gene comprises:

a) a polynucleotide which is at least 90% identical to SEQ ID NO: 1 or a fragment thereof, or

b) a polynucleotide which encodes a polypeptide which comprises an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO. 2,

wherein said isolated polynucleotide encodes a polypeptide which has homocysteine methyltransferase I activity.

Claim 12 (Withdrawn): The process of claim 11, wherein bacteria in which further gene(s) of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

Claim 13 (Withdrawn): The process of claim 11, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.

Claim 14 (Withdrawn): The process of claim 11, wherein a strain transformed with a plasmid vector is employed, and the plasmid vector carries the nucleotide sequence which codes for the *metE* gene.

Claim 15 (Withdrawn): The process of claim 11, wherein the expression of the polynucleotide(s) which code(s) for the *metE* gene is enhanced.

Claim 16 (Withdrawn): The process of claim 11, wherein the catalytic properties of the enzyme encoded by *metE* are increased.

Claim 17 (Withdrawn): The process of claim 11, wherein for the preparation of L-methionine, the coryneform microorganisms have one or more enhanced gene(s) selected from the group consisting of:

17.1 the lysC gene which codes for a feed back resistant aspartate kinase,

17.2 the gap gene which codes for glycerolaldehyde 3-phosphate dehydrogenase,

17.3 the pgk gene which codes for 3-phosphoglycerate kinase,

17.4 the pyc gene which codes for pyruvate carboxylase,

17.5 the tpi gene which codes for triose phosphate isomerase

17.6 the metA gene which codes for homoserine O-acetyltransferase

17.7 the metB gene which codes for cystathionine gamma-synthase

17.8 the aecD gene which codes for cystathionine gamma-lyase

17.9 the glyA gene which codes for serine hydroxymethyltransferase

17.10 the metY gene which codes for O-acetylhomoserine sulfhydrylase.

Claim 18 (Withdrawn): The process of claim 11, wherein for the preparation of L-methionine, the coryneform microorganisms have one or more attenuated gene(s) selected from the group consisting of:

18.1 the thrB gene which codes for homoserine kinase

18.2 the ilvA gene which codes for threonine dehydratase

18.3 the thrC gene which codes for threonine synthase

18.4 the ddh gene which codes for meso-diaminopimelate D-dehydrogenase

18.5 the pck gene which codes for phosphoenol pyruvate carboxykinase

18.6 the pgi gene which codes for glucose 6-phosphate isomerase

18.7 the poxB gene which codes for pyruvate oxidase.

Claim 19 (Withdrawn): The process of claim 11, wherein a microorganisms of the species *Corynebacterium glutamicum* is employed.

Claim 20 (Withdrawn): The process of claim 19, wherein the *Corynebacterium glutamicum* strain ATCC13032/pCREmetAE is employed.

Claim 21 (Withdrawn): The process of claim 19, wherein the *Corynebacterium glutamicum* strain ATCC13032/pCREmetAEY is employed.

Claim 22 (Withdrawn, Currently Amended): A process for the preparation of an L-methionine-containing animal feedstuffs additive comprising:

a) culturing an L-methionine-producing microorganism which comprises a *metE* gene in a fermentation medium for a time and under conditions suitable for production of L-methionine;

b) removing water from the L-methionine-containing fermentation broth (concentration);

c) removing an amount of 0 to 100 wt.% of the biomass formed during fermentation; and

d) drying the fermentation broth obtained according to b) and/or c) to obtain the animal feedstuffs additive in a powder or granule form,

wherein said *metE* gene comprises:

a) a polynucleotide which is at least 90% identical to SEQ ID NO: 1 or a fragment thereof, or

b) a polynucleotide which encodes a polypeptide which comprises an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO. 2,

wherein said isolated polynucleotide encodes a polypeptide which has homocysteine methyltransferase I activity.

Claim 23 (Withdrawn, Currently Amended): The process of claim 22, wherein said microorganism has one more ~~more~~ genes of the biosynthesis pathway of L-methionine enhanced.

Claim 24 (Withdrawn): The process of claim 22, wherein said microorganism has one more more gene(s) which reduce the formation of L-methionine attenuated or eliminated.

Claim 25 (Withdrawn): The process of claim 22, wherein expression of a polynucleotide which encodes the *metE* gene is enhanced.

Claim 26 (Withdrawn): The process of claim 22, wherein a microorganism of the species *Corynebacterium glutamicum* is employed.

Claim 27 (Withdrawn): The process of claim 26, wherein the *Corynebacterium glutamicum* strain ATCC13032/pCREmetAE is employed.

Claim 28 (Withdrawn): The process of claim 26, wherein the *Corynebacterium glutamicum* strain ATCC13032/pCREmetAEY is employed.

Claim 29 (Withdrawn): The process of claim 22, further comprising one or more of the following steps:

e) adding one or more organic substance(s), including L-methionine and/or D-methionine and/or the racemic mixture D,L-methionine, to the products obtained according to b), c) and/or d);

f) adding auxiliary substances selected from the group consisting of silicas, silicates, stearates, grits and bran to the substances obtained according to b) to e); and/or

g) converting the substances obtained according to b) to f) into a form stable in rumen, by coating them with a film-forming agent.

Claim 30 (Withdrawn): The process of claim 29, wherein a portion of the biomass is removed.

Claim 31 (Withdrawn): The process of claim 30, wherein essentially 100% of the biomass is removed.

Claim 32 (Withdrawn): The process of claim 29, wherein the water content is up to 5 wt.%.

Claim 33 (Withdrawn): The process of claim 32, wherein the water content is less than 2 wt.%.

Claim 34 (Withdrawn): The process of claim 29, wherein the film-forming agents are metal carbonates, silicas, silicates, alginates, stearates, starches, gums or cellulose ethers.

Claim 35 (Withdrawn): An animal feedstuffs additive prepared by the process of claim 22.

Claim 36 (Withdrawn): The animal feedstuffs additive of claim 35, which comprises 1 wt.% to 80 wt.% L-methionine, D-methionine, D,L-methionine or a mixture thereof, based on the dry weight of the animal feedstuffs additive.

Claim 37 (Withdrawn, Currently Amended): A process for obtaining RNA, cDNA and DNA in order to isolate nucleic acids, or polynucleotides or genes which encode a polypeptide having homocysteine methyltransferase I activity, which comprises employing a polynucleotide sequence ~~comprising~~ consisting of at least 15 consecutive nucleotides of SEQ ID NO: 1 or of the full complement of SEQ ID NO: 1 as a hybridization probe~~s~~.

Claim 38 (Currently Amended) An isolated polynucleotide comprising:

a) a polynucleotide which is at least 90% identical to SEQ ID NO: 1 ~~a~~

~~polynucleotide which encodes a polypeptide which comprises the amino acid sequence of SEQ ID NO. 2~~ or a fragment thereof ~~having homocysteine methyltransferase I activity~~, or

b) a polynucleotide which encodes a polypeptide which comprises an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO. 2 ~~and which has homocysteine methyltransferase I activity,~~

wherein said isolated polynucleotide encodes a polypeptide which has homocysteine methyltransferase I activity.

Claim 39 (Currently Amended) The isolated polynucleotide of Claim 38, which is at least 90% identical to SEQ ID NO: 1 ~~a polynucleotide which encodes a polypeptide which comprises the amino acid sequence of SEQ ID NO. 2 or a fragment thereof having homocysteine methyltransferase I activity~~.

Claim 40 (Currently Amended): The isolated polynucleotide of Claim 38, which is at least 95% identical to SEQ ID NO: 1 ~~a polynucleotide which encodes a polypeptide which comprises the amino acid sequence of SEQ ID NO. 2~~ or a fragment thereof ~~having homocysteine methyltransferase I activity~~.

Claim 41 (Currently Amended): The isolated polynucleotide of Claim 38, which is at least ~~90%~~ 99% identical to the polynucleotide of SEQ ID NO: 1 or a fragment thereof ~~encoding a polypeptide having homocysteine methyltransferase I activity~~.

Claim 42 (Currently Amended): The isolated polynucleotide of Claim 38, which is ~~at least 95% identical to the polynucleotide of~~ SEQ ID NO: 1 or a fragment thereof ~~encoding a polypeptide having homocysteine methyltransferase I activity~~.

Claim 43 (Currently Amended) The isolated polynucleotide of Claim 38, which comprises the polynucleotide of SEQ ID NO: 1 ~~or a fragment thereof encoding a polypeptide having homocysteine methyltransferase I activity~~.

Claim 44 (Previously Presented): The isolated polynucleotide of Claim 38, which encodes a polypeptide comprising an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO. 2 or a fragment thereof having homocysteine methyltransferase I activity.

Claim 45 (Previously Presented): The isolated polynucleotide of Claim 38, which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO: 2 or a fragment thereof having homocysteine methyltransferase I activity.

Claim 46 (Previously Presented) The isolated polynucleotide of Claim 38, which is RNA.

Claim 47 (Previously Presented): A vector comprising the isolated polynucleotide of Claim 38.

Claim 48 (Previously Presented) The vector of Claim 47, further comprising one or more promoter(s), regulation region(s), ribosome binding site(s), or expression cassette(s).

Claim 49 (Previously Presented): The vector of Claim 47, which is capable of replication in a coryneform bacterium.

Claim 50 (Previously Presented): A host cell comprising the isolated polynucleotide of Claim 38.

Claim 51 (Previously Presented): The host cell of Claim 50 comprising more than one copy of said isolated polynucleotide.

Claim 52 (Previously Presented): The host cell of Claim 50, wherein said isolated polynucleotide is present on a plasmid.

Claim 53 (Previously Presented): The host cell of Claim 50, wherein said isolated polynucleotide is integrated in the chromosome.

Claim 54 (Previously Presented): The host cell of Claim 50, which is a coryneform bacterium.

Claim 55 (Previously Presented): The host cell of Claim 50, which is *Corynebacterium glutamicum*.

Claim 56 (Previously Presented): *Escherichia coli* strain DHαmcr/pCREmetAE deposited as DSM 14352 at the Deutsche Sammlung für Mikroorganismen und Zellkulturen (German Collection of Microorganisms and Cell Cultures), Braunschweig, Germany.

Claim 57 (Previously Presented): *Escherichia coli* strain DHαmcr/pCREmetAEY deposited as DSM 14353 at the Deutsche Sammlung für Mikroorganismen und Zellkulturen (German Collection of Microorganisms and Cell Cultures), Braunschweig, Germany.

Claim 58 (Previously Presented) An isolated polynucleotide which is the full complement of the isolated polynucleotide of Claim 38.

Claim 59 (Currently Amended) An isolated polynucleotide ~~comprising~~ consisting of at least 15 consecutive nucleotides of SEQ ID NO: 1.

Claim 60 (Currently Amended) An isolated polynucleotide ~~comprising~~ consisting of at least 15 consecutive nucleotides of the full complement of SEQ ID NO: 1.